Detection of fim, pap, sfa and afa Adhesin-Encoding Operons in Escherichia coli Strains Isolated from Urinary Tract Infections

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ABSTRACT
Background and objectives: Urinary tract infections (UTIs) are one of the most common infectious diseases caused by bacteria. The primary etiologic agent of UTIs is Escherichia coli. Uropathogenic E.coli (UPEC) strains have a number of specific virulence factors, which can worsen UTIs. This study was performed to detect fim, pap, sfa and afa genes among E.coli strains isolated from UTIs.

Methods: A total of 100 E. coli isolates from patients with UTI was collected between June and December 2015 from Mosavi and Sayyad Shirazi hospitals in Gorgan, Iran. All bacterial isolates were identified via standard biochemical testing and Gram straining. Presence of the genes was assessed by polymerase chain reaction.

Results: The frequency of the fim, pap, sfa and afa genes was 100%, 79%, 69% and 8%, respectively. All isolates contained at least one virulence gene. Prevalence of multiple adhesion genes was 6% for all genes and 65% for three genes (fim, pap and sfa) together. In addition, the frequency of the fim gene was significantly higher than that of the other genes (P<0.0001).

Conclusion: The results of this study indicate the high prevalence of virulence factors that can enhance pathogenicity of E. coli. Therefore, these factors could be used as diagnostic markers or vaccine targets.

Keywords: Virulence factors, Urinary tract infection, Uropathogenic Escherichia coli.
INTRODUCTION

Urinary tract infections (UTIs) are inflammatory diseases caused by various pathogens, which alter the correct functioning of the urinary system (1). Escherichia coli is the major cause of UTI and the predominant facultative member of the normal human intestinal flora. The bacterium accounts for more than 80% of all UTI incidents (2). UTI comprises a range of disorders including cystitis and pyelonephritis, which are characterized by presence of microorganisms such as E. coli in the urinary tract (3, 4). Only a few E. coli strains have the potential to cause UTIs, which are classified as uropathogenic E. coli (UPEC) strains (5). UPECs express a multitude of virulence factors such as pili or fimbrae, which break the inertia of the mucosal barrier (6). The ability of these bacteria to adhere to host epithelial cells is considered as a prerequisite for the establishment of infection (7). Pyelonephritis-associated pili or P fimbrae (pap), type 1 fimbrae, afimbrial adhesin I (afaI), hemolysin (hly), cytotoxic necrotizing factor 1 (cnf 1), aerobactin (aer) and S fimbrae adhesion (sfa) are the most important virulence genes in UPEC strains, which are associated with severe UTI (8, 9). These virulence factors help the microorganism colonize host surfaces, avoid and/or subvert host defense mechanisms, damage and/or invade host cells and tissues and incite a noxious inflammatory response, thereby leading to a clinical disease (10). UPECs generally possess type 1 and P fimbrae (11). The adhesive subunit of type 1 fimbrae, FimH, is a major determinant, which has high tropism for urinary tract receptors; thus, FimH adhesion is important for colonization of E. coli in different niches (1). E. coli P fimbrae are mannose-resistant hemagglutinins predominant at the cell surface, which are associated with colonization of upper urinary tract and binding to vascular endothelium of the kidney, causing pyelonephritis. The S fimbrae is a mannose-resistant adhesin encoded by the sfa operon that recognizes α-sialyl-β-2, 3-galactose receptors in humans. Presence of S fimbrae is correlated with pathogenicity of E. coli in human meningitis and septicemia (12, 13). Pathogenic E. coli strains associated with intestinal and extra intestinal infections in humans and animals are reported to express operons of the afa family (14). The afimbrial adhesin is a mannose-resistant, P-independent, X-binding adhesin, encoded by the afa-1 operon that mediates the specific binding to uroepithelial cells and human erythrocyte receptors. The afa operon shows a high degree of heterogeneity among UPEC strains with certain subtypes being predominantly present in pyelonephritis as well as in other UTIs (15). The aim of this study was to detect the virulence genes of E. coli strains isolated from UTIs in Gorgan, Iran.

MATERIAL AND METHODS

A total of 100 E. coli strains from patients with UTI were collected between June and December 2015 from Mosavi and Sayyad Shirazi hospitals in Gorgan, Iran. The bacterial isolates were identified by Gram staining and biochemical tests, such as catalase, oxidase, indole production, citrate utilization, triple iron sugar, and methyl red-Voges Proskauer as described previously (16). The bacteria were maintained in brain heart infusion broth (Merck, Germany) with glycerol and stored at −70 °C for further studies.

Bacterial strains were sub-cultured overnight in brain heart infusion broth and genomic DNA was extracted from typical E. coli colonies using the phenol chloroform extraction method. To extract the DNA from E. coli strains, 1 ml cell suspension was centrifuged and the pellet was resuspended in lysis buffer (Sinnagen, Iran) containing proteinase K and SDS. After incubating the mixture at 65 °C for 60 min, phenol: chloroform: isoamyl alcohol (25:24:1) (Merck, Germany) was added and the suspension was shaken and centrifuged at 12000 g at 22 °C for 10 min. The supernatant was transferred to a new tube and then mixed with phenol-chloroform. The mixture was centrifuged at 9000 g for 10 min and the supernatant containing DNA was precipitated with 95% ethanol and centrifuged as described above. The pellet was washed twice with 70 % cold ethanol (-20 °C). Finally, the precipitate containing DNA was air-dried and dissolved in 50 μl of deionized distilled water and was stored at -20 °C as a template DNA stock (17).

Specific primers were used to detect some virulence factors (fim, pap, sfa, and afa) in E. coli isolates from patients with UTI. Primers for the adhesin genes were first established individually using a template DNA from
was used for statistical analysis and P-values less than 0.05 were considered statistically significant.

RESULTS

Figure 1 shows the results of gel electrophoresis for the detection of the adhesin genes (fim, pap, saf and afa). The most common virulence genes in the isolates were the fim gene (100%) followed by the pap gene (79%), the saf gene (69%) and the afa gene (8%). The frequency of the fim gene was significantly higher than that of the other genes (P<0.0001).

All isolates harbored the adhesin genes either singly or in combination. Six isolates (6%) were positive for all genes and 65 isolates (65%) were positive for the fim, pap and saf genes (Table 3).

Table 1- The specific primers used for amplification of fimbriae genes in E. coli strains isolated from UTI

<table>
<thead>
<tr>
<th>Gene</th>
<th>Sequence (5’ to 3’)</th>
<th>Size, bp</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>fim</td>
<td>GCTGTGATGTTTCTGCTGTTAAAACGAGGCGGTATTGGTG</td>
<td>167</td>
<td>(18)</td>
</tr>
<tr>
<td>saf</td>
<td>CTCGGAGAAAATCTGGGATCGGAGGTAAATTACCAACCTGGCA</td>
<td>410</td>
<td>(19)</td>
</tr>
<tr>
<td>afa</td>
<td>GCTGGGCAGCAAACATGATACCTCTC</td>
<td>750</td>
<td>(12)</td>
</tr>
<tr>
<td>pap</td>
<td>GACGCTTGGACTGCAAGGGTGCTGTGTCGGC</td>
<td>328</td>
<td>(20)</td>
</tr>
</tbody>
</table>

Table 2- PCR thermocycling conditions for detection of the virulence (fimbriae) genes in UPEC strains

<table>
<thead>
<tr>
<th>Gene</th>
<th>PCR program</th>
<th>PCR reaction mixture (25 μl)</th>
</tr>
</thead>
<tbody>
<tr>
<td>fim</td>
<td>1 cycle: 95°C ------------ 5 min</td>
<td>2.5 μl PCR buffer 10X</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 94°C ------------ 30 s</td>
<td>2 mM MgCl2</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 60°C ------------ 60 s</td>
<td>0.2 mM dNTP</td>
</tr>
<tr>
<td>saf</td>
<td>1 cycle: 72°C ------------ 30 s</td>
<td>1.25 U TaqDNA polymerase</td>
</tr>
<tr>
<td></td>
<td>3 μl DNA template</td>
<td></td>
</tr>
<tr>
<td>afa</td>
<td>1 cycle: 95°C ------------ 4 min</td>
<td>2.5 μl PCR buffer 10X</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 95°C ------------ 30 s</td>
<td>2.3 mM MgCl2</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 53°C ------------ 30 s</td>
<td>0.4 mM dNTP</td>
</tr>
<tr>
<td></td>
<td>72°C ------------ 40 s</td>
<td>10 Pmol of each primers F &amp; R</td>
</tr>
<tr>
<td></td>
<td>1 cycle: 72°C ------------ 3 min</td>
<td>1.25 U TaqDNA polymerase</td>
</tr>
<tr>
<td></td>
<td>3 μl DNA template</td>
<td></td>
</tr>
<tr>
<td>pap</td>
<td>1 cycle: 72°C ------------ 7 min</td>
<td>2.5 μl PCR buffer 10X</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 95°C ------------ 4 min</td>
<td>2.3 mM MgCl2</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 94°C ------------ 1 min</td>
<td>0.2 mM dNTP</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 65°C ------------ 1 min</td>
<td>20 Pmol of each primers F &amp; R</td>
</tr>
<tr>
<td></td>
<td>35 cycle: 72°C ------------ 3 min</td>
<td>1.25 U TaqDNA polymerase</td>
</tr>
<tr>
<td></td>
<td>1 cycle: 72°C ------------ 4 min</td>
<td>3 μl DNA template</td>
</tr>
</tbody>
</table>
detection of virulence factors. In this study, fim was the predominant gene (100%) in the E. coli isolates compared to the pap, sfa, and afa genes. These results are consistent with results of previous studies (5, 19, 20). Garofalo et al. studied 18 UPEC isolates collected from females and found that the fim gene was present in all isolates (23). In an other study, Watts et al. reported presence of the fimH gene in 98% of E. coli strains isolated from patients with UTI (24). Rahdar et al. evaluated the distribution of virulence genes among UPEC strains and reported that 95% of the isolates contained the fim gene (7). These findings may indicate the crucial role of this gene in the virulence of E. coli strains causing UTI. 

In this study, the frequency of the pap and sfa virulence genes was 79% and 69%, respectively. Saki et al. also indicated the high frequency of these virulence genes in patients with UTI in Iran (5). Some studies reported the high frequency of combined pap and sfa genes.
The high number of samples containing the pap and sfa genes together could be due to the localization of these genes on the same pathogenicity island in UPEC strains (15, 26). Similar to our results, previous studies on the frequency of the sfa and afia gene combination among UPEC isolates reported that this gene combination is either absent or less documented (15, 19). In the present study, 65% of the strains carried the fim, pap and sfa genes together. This is in agreement with findings of a recent study by Shetty et al., which stated that presence of strains with multiple adhesin genes might further increase the risk for development of UTI, particularly in women (15).

CONCLUSION
We speculate that the high prevalence of the fim, pap, and sfa operons may be responsible for UTIs in the study area. High prevalence of virulence factors can enhance the capacity of UPEC strains for colonization of the urogenital tract, resulting in increased bacterial attachment to target cells and increased pathogenicity. Thus, these genes could be targeted for vaccine production for prevention of E. coli infections. Further studies are required to identify virulence factors of E. coli strains causing UTIs and to determine the pathophysiology of these infections.

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CONFLICT OF INTEREST
The authors declare that there is no conflict of interest.

REFERENCES